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Lucas 09/813,453


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FILE COVERS 1907 - 1 May 2003  VOL 138 ISS 18
FILE LAST UPDATED: 30 Apr 2003  (20030430/ED)

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.


=> d stat que
L1          336 SEA FILE=REGISTRY (PANTOTHENATE/BI OR PANTOTHENATO/BI OR
                PANTOTHENIC/BI)
L2           37 SEA FILE=REGISTRY COAX/BI
L3         4306 SEA FILE=REGISTRY (ANTIBIOTIC/BI OR ANTIBIOTICS/BI)
L4          242 SEA FILE=REGISTRY ANTIBACTERIAL/BI
L5            3 SEA FILE=REGISTRY YACB/BI
L6         7149 SEA FILE=HCAPLUS L1 OR PANTOTHENATE?
L7              SEL  L2 1- CHEM :      106 TERMS
L8           80 SEA FILE=HCAPLUS L7
L9           80 SEA FILE=HCAPLUS L8 OR COAX
L10      226357 SEA FILE=HCAPLUS L3 OR ANTIBIOTIC?
L11       66282 SEA FILE=HCAPLUS L4 OR ANTIBACTERIA?
L12        2209 SEA FILE=HCAPLUS L5 OR YACB OR YAC(W)B OR YEAST(W)ARTIFICIAL(W)
                CHROMOSOME?
L13         535 SEA FILE=HCAPLUS L6 AND (L10 OR L11)
L14          23 SEA FILE=HCAPLUS (L9 OR L12) AND BACILLUS(W)SUBTILIS
L15           2 SEA FILE=HCAPLUS L13 AND L14


=> d ibib abs hitrn l15 1-2

L15  ANSWER 1 OF 2  HCAPLUS  COPYRIGHT 2003 ACS
ACCESSION NUMBER:         2002:157991  HCAPLUS
DOCUMENT NUMBER:          136:194232
TITLE:                    Microorganisms and assays for the identification of
                          antibiotics acting on the pantothenate
                          kinase encoded by the coaX gene
INVENTOR(S):              Yocum, R. Rogers; Patterson, Thomas A.
PATENT ASSIGNEE(S):       Omnigene Bioproducts, Inc., USA
SOURCE:                   PCT Int. Appl., 128 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   2
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PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002016601	A2	20020228	WO 2001-US26531	20010824
WO 2002016601	A3	20030123		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2002168681	A1	20021114	US 2001-813453	20010320
AU 2001085276	A5	20020304	AU 2001-85276	20010824

PRIORITY APPLN. INFO.:

US 2000-227860P	P	20000824
US 2001-813453	A	20010320
WO 2001-US26531	W	20010824

AB The present invention features methods for the identification of compds. and compns. useful as **antibiotics** and **antibacterial** agents. In particular, the invention features methods for the identification of modulators of a previously unidentified target protein, termed **CoaX**. High-throughput assay systems are featured as well as assay kits for the identification of **CoaX** modulators. Also featured are **coaX** nucleic acid mols. and purified **CoaX** proteins, as well as recombinant vectors and microorganisms including the gene, **coaX**. The first **pantothenate** kinase gene of **Bacillus subtilis**, coaA, was identified by sequence homol. The coaA gene was found to be dispensable for growth, indicating the presence of a second **pantothenate** kinase gene. Deletion of coaA and **coaX** was lethal to **Bacillus subtilis** . The gene coaA **pantothenate** kinase is the conventional **pantothenate** kinase, but sequence homologs of the **coaX** gene were found in a no. of human pathogens. An Escherichia coli host contg. a temp.-sensitive allele of the coaA gene is developed for use as a host for foreign **coaX** genes for use in **antibiotic** screening. The coaA gene product is inactive at >43.degree.. Growth at elevated temps. is therefore dependent upon the **coaX** gene product.

IT **401552-89-4 401552-90-7 401552-91-8**
401552-92-9 401552-93-0 401552-94-1
401552-95-2 401552-96-3 401552-97-4
401552-98-5 401552-99-6 401553-00-2
401553-01-3 401553-02-4 401553-03-5
401553-04-6 401553-05-7 401553-06-8
401553-07-9 401553-08-0 401553-09-1
401553-10-4 401553-11-5 401553-12-6
401553-13-7 401553-14-8 401553-15-9
401553-16-0 401553-17-1 401553-18-2
401553-19-3 401553-20-6
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence, as antibitic target; microorganisms and assays for identification of **antibiotics** acting on **pantothenate** kinase encoded by **coaX** gene)

IT **9026-48-6, Pantothenate** kinase
RL: BSU (Biological study, unclassified); BIOL (Biological study)

Searched by M. Smith

(**antibiotics** acting on; microorganisms and assays for identification of **antibiotics** acting on **pantothenate** kinase encoded by **coaX** gene)

IT **79-83-4D**, Pantothenic acid, analogs, derivs.
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(in assays for **antibiotics** blocking biosynthesis of pantothenic acid; microorganisms and assays for identification of **antibiotics** acting on **pantothenate** kinase encoded by **coaX** gene)

L15 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1997:748948 HCAPLUS
DOCUMENT NUMBER: 128:150233
TITLE: The complete genome sequence of the gram-positive bacterium Bacillus subtilis
AUTHOR(S): Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A. M.; Alloni, G.; Azevedo, V.; Bertero, M. G.; Bessieres, P.; Bolotin, A.; Borchert, S.; Borriss, R.; Boursier, L.; Brans, A.; Braun, M.; Brignell, S. C.; Bron, S.; Brouillet, S.; Bruschi, C. V.; Caldwell, B.; Capuano, V.; Carter, N. M.; Choi, S.-K.; Codani, J.-J.; Connerton, I. F.; Cummings, N. J.; Daniel, R. A.; Denizot, F.; Devine, K. M.; Dusterhoft, A.; Ehrlich, S. D.; Emmerson, P. T.; Entian, K. D.; Errington, J.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim, S.-Y.; Glaser, P.; Goffeau, A.; Golightly, E. J.; Grandi, G.; Guiseppi, G.; Guy, B. J.; Haga, K.; et al.
CORPORATE SOURCE: Unite de Biochemie Microbienne, Inst. Pasteur, Paris, 75724, Fr.
SOURCE: Nature (London) (1997), 390(6657), 249-256
CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER: Macmillan Magazines
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Bacillus subtilis is the best-characterized member of the gram-pos. bacteria. Its genome of 4,214,810 base pairs comprises 4100 protein-coding genes. Of these protein-coding genes, 53% are represented once, while a quarter of the genome corresponds to several gene families that have been greatly expanded by gene duplication, the largest family contg. 77 putative ATP-binding transport proteins. In addn., a large proportion of the genetic capacity is devoted to the utilization of a variety of carbon sources, including many plant-derived mols. The identification of 5 signal peptidase genes, as well as several genes for components of the secretion app., is important given the capacity of Bacillus strains to secrete large amts. of industrially important enzymes. Many of the genes are involved in the synthesis of secondary metabolites, including antibiotics, that are more typically assocd. with Streptomyces species. The genome contains .gtoreq.10 prophages or remnants of prophages, indicating that bacteriophage infection has played an important evolutionary role in horizontal gene transfer, in particular in the propagation of bacterial pathogenesis.

=> d stat que
L1 336 SEA FILE=REGISTRY (PANTOTHENATE/BI OR PANTOTHENATO/BI OR PANTOTHENIC/BI)
L2 37 SEA FILE=REGISTRY COAX/BI

Searched by M. Smith

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L3          4306 SEA FILE=REGISTRY (ANTIBIOTIC/BI OR ANTIBIOTICS/BI)
L4           242 SEA FILE=REGISTRY ANTIBACTERIAL/BI
L5             3 SEA FILE=REGISTRY YACB/BI
L6          7149 SEA FILE=HCAPLUS L1 OR PANTOTHENATE?
L7               SEL  L2 1- CHEM :     106 TERMS
L8            80 SEA FILE=HCAPLUS L7
L9            80 SEA FILE=HCAPLUS L8 OR COAX
L10       226357 SEA FILE=HCAPLUS L3 OR ANTIBIOTIC?
L11        66282 SEA FILE=HCAPLUS L4 OR ANTIBACTERIA?
L12         2209 SEA FILE=HCAPLUS L5 OR YACB OR YAC(W)B OR YEAST(W)ARTIFICIAL(W)
               CHROMOSOME?
L13          535 SEA FILE=HCAPLUS L6 AND (L10 OR L11)
L14           23 SEA FILE=HCAPLUS (L9 OR L12) AND BACILLUS(W)SUBTILIS
L15            2 SEA FILE=HCAPLUS L13 AND L14
L16           76 SEA FILE=HCAPLUS (L6 OR L9 OR L12) AND BACILLUS(W)SUBTILIS
L17           15 SEA FILE=HCAPLUS L16 AND (L10 OR L11)
L18           13 SEA FILE=HCAPLUS L17 NOT L15


=> d ibib abs hitrn l18 1-13

L18  ANSWER 1 OF 13  HCAPLUS  COPYRIGHT 2003 ACS
ACCESSION NUMBER:         2002:575221  HCAPLUS
DOCUMENT NUMBER:          137:136055
TITLE:                    Combinatorial expression libraries with individual
                          members of the library containing concatemers of
                          expression cassettes
INVENTOR(S):              Goldsmith, Neil; Sorensen, Alexandra M. P. Santana;
                          Nielsen, Soren V. S.; Naesby, Michael
PATENT ASSIGNEE(S):       Evolva Biotech A/S, Den.
SOURCE:                   PCT Int. Appl., 124 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

     PATENT NO.        KIND  DATE          APPLICATION NO.  DATE
     ---------------   ----  --------      ---------------  --------
     WO 2002059296      A2   20020801      WO 2002-DK55     20020125
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
             PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,
             UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU,
             TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH,
             CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR,
             BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.:                  DK 2001-127      A  20010125
                                        US 2001-301022P  P  20010627
AB   Combinatorial gene expression libraries in which individual clones contain
     large nos. of expression cassettes and methods of constructing such
     libraries are described.  Each member of the library contains a large no.
     of expression cassettes that are randomly selected from a pool of
     cassettes during the construction of the library.  Individual expression
     cassettes are flanked by a common pair of restriction sites and have the
     same promoter and terminator for uniform regulation of expression of the
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cloned inserts. The library of concatemers is created from a library of individual clones. This primary library, typically a cDNA library, has the individual cassette and its flanking restriction sites flanked by a second pair of restriction sites. The cassettes are released from the library and ligated into concatemers that are then cloned into a vector capable of stabilizing large inserts, esp. artificial chromosomes. The variability within the combinatorial library can be increased by using cDNA libraries from multiple sources. Such libraries are useful in discovery of novel or modified metabolic pathways leading to the prodn. of novel compds. for e.g. drug discovery and to the prodn. of known compds. in novel quantities or in novel compartments of the cells. The expression libraries in particular are composed of host cells capable of coordinated and controllable expression of large nos. of heterologous genes in the host cells.

IT **6379-56-2**, Hygromycin
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(resistance to, as selectable marker; combinatorial expression libraries with individual members of library contg. concatemers of expression cassettes)

L18 ANSWER 2 OF 13 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:256452 HCAPLUS
DOCUMENT NUMBER: 136:290803
TITLE: Preparation of surfactin by fermentation of **Bacillus subtilis** SD901 with soybean flour
INVENTOR(S): Yoneda, Tadashi; Miyota, Yoshiaki; Furuya, Kazuo; Tsuzuki, Toshi
PATENT ASSIGNEE(S): Showa Denko K.K., Japan
SOURCE: PCT Int. Appl., 39 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002026961	A2	20020404	WO 2001-JP8568	20010928
WO 2002026961	A3	20030320		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 2001092304	A5	20020408	AU 2001-92304	20010928
JP 2002176993	A2	20020625	JP 2001-300369	20010928

PRIORITY APPLN. INFO.:
JP 2000-300300 A 20000929
US 2000-258560P P 20001229
WO 2001-JP8568 W 20010928

AB A process for producing Surfactin, comprising culturing a microorganism of the genus Bacillus in a liq. culture medium contg. flour of beans such as soybean or an ext. thereof as a nitrogen source and accumulating Surfactin in the culture broth, and a microorganism of the genus Bacillus which have

an activity to produce a crude Surfactin in a concn. of from 8 to 50 g/L on culturing for 20 to 90 h.

IT **63-91-2P**, L-Phenylalanine, biological studies
RL: BMF (Bioindustrial manufacture); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation)
(amino acid in medium; prepn. of surfactin by fermn. of **Bacillus subtilis** SD901 with soybean flour)

IT **79-83-4P**, Pantothenic acid
RL: BMF (Bioindustrial manufacture); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation)
(vitamin in medium; prepn. of surfactin by fermn. of **Bacillus subtilis** SD901 with soybean flour)

L18 ANSWER 3 OF 13 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:142927 HCAPLUS
DOCUMENT NUMBER: 136:194227
TITLE: High throughput screen for inhibitors of the folate biosynthetic pathway in bacteria
INVENTOR(S): Murphy, Christopher
PATENT ASSIGNEE(S): Millennium Pharmaceuticals Inc., USA
SOURCE: PCT Int. Appl., 31 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002014559	A2	20020221	WO 2001-US41665	20010810
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2002164602	A1	20021107	US 2001-925824	20010809
AU 2001085429	A5	20020225	AU 2001-85429	20010810

PRIORITY APPLN. INFO.:
US 2000-224925P P 20000811
WO 2001-US41665 W 20010810

AB Methods for identifying compds. that are inhibitors of bacterial tetrahydrofolate biosynthesis are disclosed. The invention is based upon the discovery that the activity of promoters of certain genes is increased in the presence of compds. that inhibit B. subtilis tetrahydrofolate biosynthesis. Thus, compds. that inhibit tetrahydrofolate biosynthesis can be identified by their ability to increase the activity of the **Bacillus subtilis** panB promoter. Various promoters can be used in the invention, provided that the activity of the promoter is upregulated by a tetrahydrofolate biosynthesis inhibitor, such as trimethoprim or sulfonamide. Such compds. can be used as lead compds. in methods for prepg. **antibacterial** agents for treating bacterial infections (e.g., in humans, animals, and plants). The disclosed methods allow for high throughput screening of libraries of test compds.

IT **9023-49-8**, **Pantothenate** synthetase
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)

(in genetic promoter detn.; high throughput screen for inhibitors of folate biosynthetic pathway in bacteria by detg. their ability to affect activity of genetic promoters such as panB promoter)

L18 ANSWER 4 OF 13 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:142868 HCAPLUS
DOCUMENT NUMBER: 136:178954
TITLE: Enhanced homologous recombination mediated by phage .lambda. recombination proteins
INVENTOR(S): Court, Donald L.; Yu, Daiguan; Lee, E-Chiang; Ellis, Hilary M.; Jenkins, Nancy A.; Copeland, Neal G.
PATENT ASSIGNEE(S): The Government of the United States of America, as Represented by the Secretary, Department of Health and Human Services, the National Institutes of Health and Human Services, USA
SOURCE: PCT Int. Appl., 124 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002014495	A2	20020221	WO 2001-US25507	20010814
WO 2002014495	A3	20020801		
WO 2002014495	B1	20021010		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

AU 2001083377	A5	20020225	AU 2001-83377	20010814

PRIORITY APPLN. INFO.:
US 2000-225164P P 20000814
US 2001-271632P P 20010226
WO 2001-US25507 W 20010814

AB Disclosed herein are methods for generating recombinant DNA mols. in cells using homologous recombination mediated by recombinases and similar proteins. Such recombinases include the .lambda. proteins Beta, Exo, and Gam. The phage .lambda. recombinases are operably linked to a de-repressible promoter such as the .lambda. PL promoter, which is activated by temp. shift, thereby leading to expression of the .lambda. recombinases. Methods are also provided by inducing homologous recombination using single-stranded DNA mols., by introducing into the cell DNA capable of undergoing homologous recombination, and a single-stranded DNA-binding protein capable of promoting homologous recombination. Such single-stranded DNA binding proteins include .lambda. Beta, RecT, P22 Erf, and Rad52. The methods promote high efficiency homologous recombination in bacterial cells, and in eukaryotic cells such as mammalian cells. The methods are useful for cloning, the generation of transgenic and knockout animals, and gene replacement. The methods are also useful for subcloning large DNA fragments without the need for restriction enzymes. The methods are also useful for repairing single or multiple base mutations to wild type or creating specific mutations in the genome. Also disclosed are bacterial strains which are useful for

high-efficiency homologous recombination. Thus, a highly efficient recombination for manipulating BAC DNA in Escherichia coli is described which uses a defective .lambda. prophage to supply functions that protect and recombine the electroporated linear DNA targeting cassette with the BAC sequence.

L18 ANSWER 5 OF 13 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:89878 HCAPLUS
DOCUMENT NUMBER: 136:156403
TITLE: Methods for identifying therapeutic targets for treating infectious disease
INVENTOR(S): Shepard, Michael H.; Lackey, David B.; Cathers, Brian E.; Sergeeva, Maria V.
PATENT ASSIGNEE(S): Newbiotics, Inc., USA
SOURCE: PCT Int. Appl., 503 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002007780	A2	20020131	WO 2001-US23095	20010720
WO 2002007780	A3	20030220		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.:
US 2000-219598P P 20000720
US 2000-244953P P 20001101
US 2001-276728P P 20010316

AB This invention provides methods and systems to identify enzymes that act as enzyme-catalyzed therapeutic activators and the enzymes identified by these methods. Also provided by this invention are compds. activated by the enzymes as well as compns. contg. these compds.

IT **9023-49-8**, E.C. 6.3.2.1 **9026-48-6**, E.C. 2.7.1.33
RL: CAT (Catalyst use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(identifying intrinsic enzyme-catalyzed therapeutic activators as targets for treating infectious disease)

L18 ANSWER 6 OF 13 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:10213 HCAPLUS
DOCUMENT NUMBER: 136:69139
TITLE: Bioactive food complex, method for making bioactive food complex product and method for controlling disease
INVENTOR(S): Villamar, Daniel F.; Moriarty, David J. W.
PATENT ASSIGNEE(S): Acuabiotec Llc, USA
SOURCE: PCT Int. Appl., 38 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002000035	A1	20020103	WO 2001-US16489	20010622
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 2001068078	A5	20020108	AU 2001-68078	20010622
PRIORITY APPLN. INFO.:			US 2000-213538P P	20000623
			WO 2001-US16489 W	20010622

AB A bioactive food complex product, method for prepg. a bioactive food complex product and method for controlling disease uses probiotics and quorum sensing inhibitors such as inhibitory furanones and other bioactive compds. included in both the continuous and dispersed phases of a bioactive food complex product. The product is comprised of a solids-in-oil or an oil-in-solids emulsion forming a first emulsion that is itself emulsified in polymer forming oil-in-polymer or solids-in-polymer emulsion complex. The bioactive complex is formed of two emulsions with the first emulsion comprising the dispersed phase and a hydrocolloid polymer serving as the continuous phase. The second emulsion complex is then crosslinked to form a phys. stable matrix. The bioactive food complex or the first emulsion of the bioactive food complex then serve to deliver different bioactive components including probiotic bacteria and quorum sensing inhibitor mols. to the digestive tract and environment of animals such as shrimp or fish or other livestock raised com. to effectively control bacterial disease by a novel combination of mechanisms including: competitive exclusion, direct inhibition, digestion of cell-to-cell signaling mols. and direct inhibition of homoserine lactone and (acyl) homoserine lactone-regulated processes of pathogenic bacteria. Thus, effective disease prevention and control is accomplished through the novel combined delivery and use of probiotic bacteria and quorum sensing inhibitory furanones.

IT **79-57-2**, Terramycin **79-83-4**, D-Pantothenic acid
RL: FFD (Food or feed use); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(bioactive food complex, method for making bioactive food complex product and method for controlling disease)

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 7 OF 13 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:897198 HCAPLUS
DOCUMENT NUMBER: 134:81633
TITLE: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis
AUTHOR(S): Takami, Hideto; Nakasone, Kaoru; Takaki, Yoshihiro; Maeno, Go; Sasaki, Rumie; Masui, Noriaki; Fuji, Fumie; Hirama, Chie; Nakamura, Yuka; Ogasawara, Naotake; Kuhara, Satoru; Horikoshi, Koki
CORPORATE SOURCE: Deep-Sea Microorganisms Research Group, Japan Marine

Science and Technology Center, Kanagawa, 237-0061, Japan
SOURCE: Nucleic Acids Research (2000), 28(21), 4317-4331
CODEN: NARHAD; ISSN: 0305-1048
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The 4,202,353 bp genome of the alkaliphilic bacterium Bacillus halodurans C-125 contains 4066 predicted protein coding sequences (CDSs), 2141 (52.7%) of which have functional assignments, 1182 (29%) of which are conserved CDSs with unknown function, and 743 (18.3%) of which have no match to any protein database. Among the total CDSs, 8.8% match sequences of proteins found only in Bacillus subtilis and 66.7% are widely conserved in comparison with the proteins of various organisms, including B. subtilis. The B. halodurans genome contains 112 transposase genes, indicating that transposases have played an important evolutionary role in horizontal gene transfer and also in internal genetic rearrangement in the genome. Strain C-125 lacks some of the necessary genes for competence, such as comS, srfA, and rapC, supporting the fact that competence has not been demonstrated exptl. in C-125. There is no paralog of tupA, encoding teichuronopeptide, which contributes to alkaliphily, in the C-125 genome and an ortholog of tupA cannot be found in the B. subtilis genome. Out of 11 .sigma. factors which belong to the extracytoplasmic function family, 10 are unique to B. halodurans, suggesting that they may have a role in the special mechanism of adaptation to an alk. environment. The sequence has been deposited in DDBJ/EMBL/GenBank with the Accession Nos. AP001507-AP001520.
REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 8 OF 13 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:116908 HCAPLUS
DOCUMENT NUMBER: 132:150908
TITLE: Methods for increasing the solubility of nutritional materials using probiotic lactic acid-producing bacteria
INVENTOR(S): Farmer, Sean
PATENT ASSIGNEE(S): Ganeden Biotech, Inc., USA
SOURCE: PCT Int. Appl., 43 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000007606	A2	20000217	WO 1999-US17671	19990806
WO 2000007606	A3	20000518		

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

CA 2339643	AA	20000217	CA 1999-2339643	19990806

AU 9957719	A1	20000228	AU 1999-57719	19990806
EP 1102595	A2	20010530	EP 1999-945016	19990806
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2002522393	T2	20020723	JP 2000-563291	19990806

PRIORITY APPLN. INFO.:

US 1998-95786P	P	19980807
US 1999-369016	A2	19990805
WO 1999-US17671	W	19990806

AB The present invention discloses therapeutic compns. and methods of use of probiotic, non-lactic acid-producing bacteria to increase the soly. and bioavailability of nutritional materials, preferably vitamins and minerals, within the gastrointestinal tract of an animal or human. The therapeutic compns. of the present invention preferably utilize Bacillus species, and most preferably Bacillus coagulans, as the lactic acid-producing, probiotic bacterial species. The therapeutic compns. disclosed herein may also contain one or more vitamins or minerals so as to exogenously augment the intake of these substances.

IT **79-83-4**, Pantothenic acid
RL: FFD (Food or feed use); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(methods for increasing the soly. of nutritional materials using probiotic lactic acid-producing bacteria)

L18 ANSWER 9 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER:	1993:447918 HCAPLUS
DOCUMENT NUMBER:	119:47918
TITLE:	Method for effective utilization of skipjack tuna viscera
AUTHOR(S):	Chun, Lee Soon; Lyung, Woo Kang
CORPORATE SOURCE:	Dev. Inst., Dong Won Ind. Co., S. Korea
SOURCE:	Han'guk Sikp'um Kwahakhoechi (1992), 24(1), 86-91 CODEN: HSKCAN; ISSN: 0367-6293
DOCUMENT TYPE:	Journal
LANGUAGE:	Korean

AB To develop an effective utilization method of skipjack tuna viscera, fish meal (FFMA) was prepd. by fermn. of the solid materials sepd. from autoclaved viscera with Aspergillus oryzae for 72 h and adding the concd. sol. exts. sepd. from autoclaved viscera to the fermenting solid materials during fermn. FFMA fish meal was compared with the fish meals prepd. by the Kato method (FFMN) and conventional nonfermenting method (NFM). FFMN fish meal was prepd. by fermenting the solid materials sepd. from autoclaved viscera with Aspergillus oryzae for 17 h without adding the sol. ext. The exts. from FFMA fish meal (FFMA-E) and raw viscera (RM-E) were also prepd. after digestion with proteases obtained from **Bacillus subtilis** and Aspergillus oryzae, resp., and compared with each other with respect to contents of free amino acids. The peroxide values decreased greatly and contents of vitamin B1, B2, and C significantly increased in FFMA fish meal compared with those of other fish meals. The total free amino acid content of FFMA-E was significantly higher then that of RM-E. The total free essential amino acid content also greatly increased in FFMA-E, in which threonine, methionine, and lysine showed marked increments. Almost all individual nonessential amino acids were higher in FFMA-E than in RM-E. The content of taurine, a nonprotein amino acid, greatly increased compared with other nonprotein amino acids in both exts.

IT **63-91-2**, Phenylalanine, biological studies **79-83-4**, Vitamin B3
RL: BIOL (Biological study)
(of fish meal from Aspergillus oryzae fermn.)

L18 ANSWER 10 OF 13 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1969:520780 HCAPLUS
DOCUMENT NUMBER: 71:120780
TITLE: Metabolic products of microorganisms. LXXVIII. Isolation, identification, and mehanism of action of ketomycin [(R)-3-cyclohexene-1-glyoxylic acid] and of its conversion product 3-cyclohexene-1-glycine
AUTHOR(S): Keller-Schierlein, Walter; Poralla, K.; Zaehner, Hans
CORPORATE SOURCE: Eidg. Tech. Hochsch. Zurich, Zurich, Switz.
SOURCE: Archiv fuer Mikrobiologie (1969), 67(4), 339-56
CODEN: ARMKA7; ISSN: 0003-9276
DOCUMENT TYPE: Journal
LANGUAGE: German
AB Ketomycin isolated from culture filtrates of Streptomyces strain Tu99 inhibited growth of **Bacillus subtilis**: this inhibition could be reversed competitively by homoserine, threonine, .alpha.-ketobutyrate, .alpha.-keto-.beta.-methylvalerate, .alpha.-ketoisovalerate, valine, .alpha.-ketoisocapronate, or leucine, and noncompetitively by isoleucine. Pyruvate, acetoin, and **pantothenate** had no effect on growth inhibition. Growing **Bacillus subtilis** cultures converted ketomycin to 3-cyclohexene-1-glycine and the growth inhibitory effects of this metabolite were counteracted by the same substances and in a similar manner as observed for ketomycin. In vitro, 3-cyclohexene-1-glycine production from ketomycin was catalyzed by an amino acid dehydrogenase but not by a transaminase. Ketomycin competitively inhibited an amino acid dehydrogenase which converts .alpha.-keto-.beta.-methylvalerate to isoleucine. 3-Cyclohexene-1-glycine inhibited threonine deaminase competitively with respect to threonine, which may explain the antagonistic action in vivo of threonine and possibly homoserine. At concns. 10 times higher than isoleucine, 3-cyclohexene-1-glycine only slightly inhibited the attachment of isoleucine to tRNA by isoleucyl-tRNA synthetase, explaining the noncompetitive antagonism of isoleucine in vivo. No explanation of the antagonistic effect of valine, leucine, and their immediate precursors was found.
IT **23364-22-9**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(bactericidal action of)

L18 ANSWER 11 OF 13 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1968:454300 HCAPLUS
DOCUMENT NUMBER: 69:54300
TITLE: The microbiological assay of **antibiotic** and vitamin preparations
AUTHOR(S): De Carneri, I.; Meinardi, G.
CORPORATE SOURCE: "Carlo Erba" S.p.A., Milan, Italy
SOURCE: Farmaco, Edizione Pratica (1968), 23(8), 439-46
CODEN: FRPPAO; ISSN: 0430-0912
DOCUMENT TYPE: Journal
LANGUAGE: Italian
AB A new rapid automatic turbidimetric bioassay for dosage forms of tetracycline, vitamin B12, and pantothenic acid is described. **Bacillus subtilis** is used for the **antibiotics**, and Escherichia coli for the vitamins. The growth rate is detd. in colorimeter tubes in both the presence and the absence of the test substances, which are maintained at const. temp. during the incubation period. The turbidity is detd. after 3 hrs. of incubation with

antibiotics and 5 hrs. with the vitamins. This automatic turbidimetric method compared extremely well with the classical agar plate method.

IT **60-54-8**, analysis **79-83-4**
RL: ANT (Analyte); ANST (Analytical study)
(detn. of, microbiol.)

L18 ANSWER 12 OF 13 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1966:481537 HCAPLUS
DOCUMENT NUMBER: 65:81537
ORIGINAL REFERENCE NO.: 65:15167d-e
TITLE: **Antibiotic** and sulfonamide oral preparations
PATENT ASSIGNEE(S): Instituto de Biologia y Sueroterapia S.A.
SOURCE: 7 pp.
DOCUMENT TYPE: Patent
LANGUAGE: Unavailable
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
ES 308870		19650701	ES	19650202

AB The oral prepns. contain, in an enteric coating, as well as the **antibiotic** and the sulfonamide, vitamins of the B-complex and a substitute intestinal flora. The latter comprises resistant strains of Lactobacillus acidophilus, and may also include L. lactis, L. helveticus, and L. bifidus, Streptococcus lactis, and species of B [acterium] coli, [Escherichia coli] and **Bacillus subtilis** in a nutrient medium.

IT **137-08-6**, Pantothenic acid, calcium salt
(**antibiotic** oral prepn. contg.)

IT **57-62-5**, 2-Naphthacenecarboxamide, 7-chloro-4-(dimethylamino)-1,4,4a,5,5a,6,11,12a-octahydro-3,6,10,12,12a-pentahydroxy-6-methyl-1,11-dioxo- **60-54-8**, 2-Naphthacenecarboxamide, 4-(dimethylamino)-1,4,4a,5,5a,6,11,12a-octahydro-3,6,10,12,12a-pentahydroxy-6-methyl-1,11-dioxo- **79-57-2**, 2-Naphthacenecarboxamide, 4-(dimethylamino)-1,4,4a,5,5a,6,11,12a-octahydro-3,5,6,10,12,12a-hexahydroxy-6-methyl-1,11-dioxo- **303-81-1**, Novobiocin **1400-61-9**, Nystatin
(pharmaceutical prepn. contg.)

L18 ANSWER 13 OF 13 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1959:123416 HCAPLUS
DOCUMENT NUMBER: 53:123416
ORIGINAL REFERENCE NO.: 53:22253i,22254a-d
TITLE: Erythromycin. Its mode of action
AUTHOR(S): Streightoff, Frank
CORPORATE SOURCE: Eli Lilly and Co., Indianapolis, IN
SOURCE: Butler Univ. Botan. Studies (1959), Volume Date 1958, 13, 179-214
DOCUMENT TYPE: Journal
LANGUAGE: Unavailable

AB Of nearly 100 compds. tested, none were capable of reversing the inhibition caused by erythromycin (I) of Staphylococcus aureus and the spores of **Bacillus subtilis**. Compds. in acid soln. reversed the activity of I and those in alk. soln. increased its activity. For clin. purposes the reactivation of organisms inhibited by I was favored by growing them in media with as low a pH as would be compatible with the organism. Ca **pantothenate** (II) or .beta.-alanine (III) did not reverse competitively the inhibition by I of Corynebacterium

diphtheriae, Diplococcus pneumoniae, Lactobacillus casei, S. aureus, and Streptococcus pyogenes. Both II and III reversed the inhibition of Saccharomyces cerevisiae by I. Because of soly. reasons it was not possible to compare I with p-aminobenzoic acid and sulfa drugs. There was no evidence of synthesis of a metabolite competitive with I by resistant organisms. Resistant strains of S. aureus synthesized the same amt. of I as a sensitive strain. Resistant strains of several species did not synthesize extracellular metabolite capable of reversing the action of I. No extracellular nor intracellular erythromycinase was found. I reduced the activity of the coagulase of S. aureus. Four degradation products of I were tested, desosamine (IV), cladenose, dihydroerythronolide, and erythralosamine. None had any effect on the coagulase approaching that of I. IV had no action on I and no bacteriostatic effect. IV and cladenose, degradation products of I, did not reduce the action of coagulase. I had no effect on glucose oxidase and horseradish peroxidase. The coagulase activity test is recommended as an in vitro method for testing drugs against S. aureus.

IT **79-83-4**, Pantothenic acid
(effect on erythromycin inhibition of yeast)

diphtheriae, Diplococcus pneumoniae, Lactobacillus casei, S. aureus, and Streptococcus pyogenes. Both II and III reversed the inhibition of Saccharomyces cerevisiae by I. Because of soly. reasons it was not possible to compare I with p-aminobenzoic acid and sulfa drugs. There was no evidence of synthesis of a metabolite competitive with I by resistant organisms. Resistant strains of S. aureus synthesized the same amt. of I as a sensitive strain. Resistant strains of several species did not synthesize extracellular metabolite capable of reversing the action of I. No extracellular nor intracellular erythromycinase was found. I reduced the activity of the coagulase of S. aureus. Four degradation products of I were tested, desosamine (IV), cladenose, dihydroerythronolide, and erythralosamine. None had any effect on the coagulase approaching that of I. IV had no action on I and no bacteriostatic effect. IV and cladenose, degradation products of I, did not reduce the action of coagulase. I had no effect on glucose oxidase and horseradish peroxidase. The coagulase activity test is recommended as an in vitro method for testing drugs against S. aureus.

IT **79-83-4**, Pantothenic acid
(effect on erythromycin inhibition of yeast)

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File  34:SciSearch(R) Cited Ref Sci 1990-2003/Apr W4
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File  35:Dissertation Abs Online 1861-2003/Mar
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File  40:Enviroline(R) 1975-2003/Mar
File 345:Inpadoc/Fam.& Legal Stat 1968-2003/UD=200316
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         (c) 2003  THOMSON DERWENT
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File 440:Current Contents Search(R) 1990-2003/May 01
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S1        449   (PANTOTHEN? OR COAX OR YACB OR YAC(W)B OR YEAST(W)ARTIFICI-
            AL(W)CHROMOSOME?) AND BACILLUS(W)SUBTILIS
S2        340   RD (unique items)
S3         14   S2 AND (ANTIBIOTIC? OR ANTIBACTER?)
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>>>No matching display code(s) found in file(s): 65, 345

 3/AB/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.

04699172   85004968   PMID: 6434382
  Standardization of parameters for the mycobacillin synthetase activity.
  Mukhopadhyay N K; Majumder S; Ghosh S K; Bhattacharya D; Bose S K
  Folia microbiologica (CZECHOSLOVAKIA)   1984,  29   (4)  p295-300,  ISSN
0015-5632   Journal Code: 0376757
  Document type: Journal Article
  Languages: ENGLISH
  Main Citation Owner: NLM
  Record type: Completed
  An effective method of preparation involving sonication was developed for
cell-free mycobacillin synthetase from Bacillus subtilis . The enzyme
showed optimum activity at a buffer concentration of 50 mM (Tris-HCl) and
pH 7.5. ATP and Mg2+ which were essential for synthesis showed an optimum
requirement at a ratio of 1:1. The synthetase was markedly inhibited by ADP
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whereas AMP was without any effect. ATP or ATP-generating system could not be replaced by GTP, UTP or CTP. Co2+ and Mn2+ could to some extent substitute Mg2+. Mercapto reagents inhibited the antibiotic synthesis. Exogenous addition of pantothenic acid had no effect.

3/AB/2 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

10064716 Genuine Article#: 480UA Number of References: 28
Title: Bacilysin biosynthesis by a partially-purified enzyme fraction from Bacillus subtilis (ABSTRACT AVAILABLE)
Author(s): Yazgan A; Ozcengiz G (REPRINT) ; Ozcengiz E; Kilinc K; Marahiel MA; Alaeddinoglu NG
Corporate Source: Middle E Tech Univ,Dept Biol,TR-06531 Ankara//Turkey/ (REPRINT); Middle E Tech Univ,Dept Biol,TR-06531 Ankara//Turkey/; Refik Saydam Ctr Hyg,Vaccine Prod & Res Div,TR-06100 Ankara//Turkey/; Hacettepe Univ,Dept Biochem,TR-06100 Ankara//Turkey/; Univ Marburg,Biochem FB Chem,D-35032 Marburg//Germany/
Journal: ENZYME AND MICROBIAL TECHNOLOGY, 2001, V29, N6-7 (OCT 4), P400-406
ISSN: 0141-0229 Publication date: 20011004
Publisher: ELSEVIER SCIENCE INC, 655 AVENUE OF THE AMERICAS, NEW YORK, NY 10010 USA
Language: English Document Type: ARTICLE
Abstract: Biosynthesis of dipeptide antibiotic bacilysin by a partially purified enzyme prepared from Bacillus subtilis PY79 was studied. Cell material was desintegrated by treatment with lysozyme and sonication and the extract was subjected to ammonium sulfate fractionation. Bacilysin-synthesizing enzyme activity was precipitated between 40% to 70% ammonium sulfate saturation. In vitro enzymatical synthesis of bacilysin was confirmed by performing thin layer chromatographic comparison of the antibiotic formed with the authentic bacilysin. An enzyme fraction (ca. 125 kDa) was prepared by fast flow gel permeation chromatography which was further purified by anion exchange FPLC. The enzymatic synthesis of bacilysin required either ATP or 2'-deoxy ATP and was entirely dependent on the presence of constituting amino acids. Although anticapsin, at the concentration used in enzyme assay, did not produce an inhibition zone when assayed against Staphylococcus aureus ATCC 9144, it exhibited a slight inhibition zone after incubation with the enzyme fraction in the absence of alanine under the standard assay conditions. To determine the mechanism of amino acid activation, ATP-PPi and ATP-P-i exchange reactions were performed with component amino acids L-alanine and L-anticapsin. The enzyme catalyzed ATP-PPi exchange reaction dependent on L-alanine, but did not activate L-anticapsin in this way. There was also no evidence for activation of this amino acid as an amino acid phosphate. Pantothenic acid was liberated from the enzyme fraction as determined microbiologically. Consistently, covalent binding as thioester was shown for L-alanine. These results indicated that the mechanism of bacilysin biosynthesis is not typical of the general multicarrier thiotemplate model. (C) 2001 Elsevier Science Inc. All rights reserved.

3/AB/3 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

06275648 Genuine Article#: YG667 Number of References: 49
Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis (ABSTRACT AVAILABLE)

Author(s): Kunst F (REPRINT) ; Ogasawara N; Moszer I; Albertini AM; Alloni G; Azevedo V; Bertero MG; Bessieres P; Bolotin A; Borchert S; Borriss R ; Boursier L; Brans A; Braun M; Brignell SC; Bron S; Brouillet S; Bruschi CV; Caldwell B; Capuano V; Carter NM; Choi SK; Codani JJ; Connerton IF; Cummings NJ; Daniel RA; Denizot F; Devine KM; Dusterhoft A; Ehrlich SD; Emmerson PT; Entian KD; Errington J; Fabret C; Ferrari E ; Foulger D; Fritz C; Fujita M; Fujita Y; Fuma S; Galizzi A; Galleron N ; Ghim SY; Glaser P; Goffeau A; Golightly EJ; Grandi G; Guiseppi G; Guy BJ; Haga K; Haiech J; Harwood CR; Henaut A; Hilbert H; Holsappel S; Hosono S; Hullo MF; Itaya M; Jones L; Joris B; Karamata D; Kasahara Y; KlaerrBlanchard M; Klein C; Kobayashi Y; Koetter P; Koningstein G; Krogh S; Kumano M; Kurita K; Lapidus A; Lardinois S; Lauber J; Lazarevic V; Lee SM; Levine A; Liu H; Masuda S; Mauel C; Medigue C; Medina N; Mellado RP; Mizuno M; Moestl D; Nakai S; Noback M; Noone D; OReilly M; Ogawa K; Ogiwara A; Oudega B; Park SH; Parro V; Pohl TM; Portetelle D; Porwollik S; Prescott AM; Presecan E; Pujic P; Purnelle B ;

Corporate Source: INST PASTEUR,UNITE BIOCHIM MICROBIENNE, 25 RUE DR ROUX/F-75724 PARIS 15//FRANCE/ (REPRINT); NARA INST SCI & TECHNOL,GRAD SCH BIOL SCI/NARA 63001//JAPAN/; INST PASTEUR,UNITE REGULAT EXPRESS GENET/F-75724 PARIS 15//FRANCE/; UNIV PAVIA,DIPARTIMENTO GENET & MICROBIOL/I-27100 PAVIA//ITALY/; INRA,/F-78352 JOUY EN JOSAS//FRANCE/; UNIV FRANKFURT,INST MIKROBIOL/D-60439 FRANKFURT//GERMANY/; HUMBOLDT UNIV BERLIN,INST GENET & MIKROBIOL/D-10115 BERLIN//GERMANY/; UNIV LIEGE,CTR INGN PROT, INST CHIM B6/B-4000 LIEGE//BELGIUM/; QIAGEN GMBH,/D-40724 HILDEN//GERMANY/; UNIV NEWCASTLE UPON TYNE,SCH MED, DEPT MICROBIOL IMMUNOL & VIROL SCI/NEWCASTLE UPON TYNE NE2 4HH/TYNE & WEAR/ENGLAND/; UNIV GRONINGEN,DEPT GENET/NL-9751 NN HAREN//NETHERLANDS/ ; UNIV PARIS 06,ATELIER BIOINFORMAT/F-75005 PARIS//FRANCE/; INT CTR GENET ENGN & BIOTECHNOL,AREA SCI PK/I-34012 TRIESTE//ITALY/; GENENCOR INT,/PALO ALTO//CA/94304; KRIBB,APPL MICROBIOL RES DIV, BACTERIAL MOL GENET RES UNIT/TAEJON 305600//SOUTH KOREA/; INST NATL RECH INFORMAT & AUTOMAT,/F-78153 LE CHESNAY//FRANCE/; AFRC,INST FOOD RES, READING LAB, DEPT FOOD MACROMOL SCI/READING RG6 6BZ/BERKS/ENGLAND/; UNIV OXFORD,SIR WILLIAM DUNN SCH PATHOL/OXFORD OX1 3RE//ENGLAND/; CNRS,CHIM BACTERIENNE LAB/F-13402 MARSEILLE 09//FRANCE/; TRINITY COLL DUBLIN,DEPT GENET/DUBLIN//IRELAND/; UNIV NEWCASTLE UPON TYNE,SCH MED, DEPT BIOCHEM & GENET/NEWCASTLE UPON TYNE NE2 4HH/TYNE & WEAR/ENGLAND/; NATL INST GENET,CTR RADIOISOTOPE/MISHIMA/SHIZUOKA 411/JAPAN/; FUKUYAMA UNIV,FAC ENGN, DEPT BIOTECHNOL/HIROSHIMA 72902//JAPAN/; UNIV TSUKUBA,INST BIOL SCI/TSUKUBA/IBARAKI 305/JAPAN/; UNIV CATHOLIQUE LOUVAIN,UNITE BIOCHIM PHYSIOL, FAC SCI AGRON/B-1348 LOUVAIN//BELGIUM/; NOVO NORDISK BIOTECH,/DAVIS//CA/95616; ENIRICERCHE SPA,/I-20097 SAN DONATO MILANESE/MILAN/ITALY/; UNIV TOKYO,INST MOL & CELLULAR BIOL, BUNKYO KU/TOKYO 113//JAPAN/; UNIV VERSAILLES,LAB GENOME & INFORMAT/F-78035 VERSAILLES//FRANCE/; TOKYO UNIV AGR & TECHNOL,FAC AGR/FUCHU/TOKYO 183/JAPAN/; MITSUBISHI KASEI INST LIFE SCI,/MACHIDA/TOKYO 194/JAPAN/; INST PASTEUR,SERV INFORMAT SCI/F-75724 PARIS 15//FRANCE/; UNIV LAUSANNE,INST GENET & BIOL MICROBIENNES/CH-1005 LAUSANNE//SWITZERLAND/; FREE UNIV AMSTERDAM,FAC BIOL, DEPT MOL MICROBIOL, MBW BCA/NL-1081 HV AMSTERDAM//NETHERLANDS/; CHONGJU UNIV,COLL SCI & ENGN/CHONJU//SOUTH KOREA/; UNIV PARIS 11,INST GENET & MICROBIOL, CNRS, URA 2225/F-91405 ORSAY//FRANCE/; CSIC,CTR NACL BIOTECNOL/E-28049 MADRID//SPAIN/; NATL INST BASIC BIOL,/OKAZAKI/AICHI 444/JAPAN/; GESELL ANAL TECH & CONSULTING MBH,/D-78467 CONSTANCE//GERMANY/; FAC AGRON,DEPT MICROBIOL/B-5030 GEMBLOUX//BELGIUM/; BMF,BIOTECH RES/D-69434 HIRSCHHORN//GERMANY/; SHINSHU UNIV,FAC TEXT SCI & TECHNOL, DEPT APPL BIOL/UEDA/NAGANO 386/JAPAN/; UNIV TOKYO,INST MED SCI, CTR HUMAN GENOME, MINATO KU/TOKYO 108//JAPAN/; TOKAI UNIV,SCH MARINE SCI & TECHNOL, DEPT MARINE SCI/SHIZUOKA 424//JAPAN/; COMMISS EUROPEAN COMMUNITIES,DG XII E 1, SDME 878/B-1049 BRUSSELS//BELGIUM/; AGOWA GMBH,/D-12489 BERLIN//GERMANY/

Journal: NATURE, 1997, V390, N6657 (NOV 20), P249-256
ISSN: 0028-0836 Publication date: 19971120
Publisher: MACMILLAN MAGAZINES LTD, PORTERS SOUTH, 4 CRINAN ST, LONDON, ENGLAND N1 9XW
Language: English Document Type: ARTICLE
Abstract: Bacillus subtilis Is the best-characterized member of the Gram-positive bacteria. Its genome of 4,214,810 base pairs comprises 4,100 protein-coding genes. Of these protein-coding genes, 53% are represented once, while a quarter of the genome corresponds to several gene families that have been greatly expanded by gene duplication, the largest family containing 77 putative ATP-binding transport proteins. In addition, a large proportion of the genetic capacity is devoted to the utilization of a variety of carbon sources, including many plant-derived molecules. The identification of five signal peptidase genes, as well as several genes for components of the secretion apparatus, is important given the capacity of Bacillus strains to secrete large amounts of industrially important enzymes. Many of the genes are involved in the synthesis of secondary metabolites, Including antibiotics , that are more typically associated with Streptomyces species. The genome contains at least ten prophages or remnants of prophages, indicating that bacteriophage Infection has played an important evolutionary role in horizontal gene transfer, in particular In the propagation of bacterial pathogenesis.

3/AB/4 (Item 3 from file: 34)

05876365 Genuine Article#: XD490 Number of References: 29
Title: Isolating large nested deletions in bacterial and P1 artificial chromosomes by in vivo P1 packaging of products of Cre-catalysed recombination between the endogenous and a transposed loxP site (ABSTRACT AVAILABLE)
Author(s): Chatterjee PK (REPRINT) ; Coren JS
Corporate Source: SUNY HLTH SCI CTR,DEPT MED, 750 E ADAMS ST/SYRACUSE//NY/13210 (REPRINT); DUPONT MERCK PHARMACEUT CO,EXPT STN, GENET PROGRAM/WILMINGTON//DE/19880
Journal: NUCLEIC ACIDS RESEARCH, 1997, V25, N11 (JUN 1), P2205-2212
ISSN: 0305-1048 Publication date: 19970601
Publisher: OXFORD UNIV PRESS, GREAT CLARENDON ST, OXFORD, ENGLAND OX2 6DP
Language: English Document Type: ARTICLE
Abstract: A general approach for isolating large nested deletions in P1 artificial chromosomes (PACs)and bacterial artificial chromosomes (BACs) by retrofitting with a loxP site-containing Tn10 mini-transposon is described. Cre-mediated recombination between the loxP site existing in these clones and one introduced by transposition leads to deletions and inversions of the DNA between these sites. Large deletions are selectively recovered by transducing the retrofitted PAC or BAC clones with P1 phage. The requirement that both loxP sites in the cointegrate be packaged into a P1 head ensures that only large deletions are rescued. PCR analyses identified these deletions as products of legitimate recombination between loxP sites mediated by Cre protein. BACs produce deletions much more efficiently than PACs although the former cannot be induced to greater than unit copy in cells. Mammalian cell-responsive antibiotic resistance markers are introduced as part of the transposon into genomic clone deletions for subsequent functional analysis. Most importantly, the loxP site retrofitting and P1 transduction can be performed in the same bacterial host containing these clones directly isolated from PAC or BAC libraries. These procedures should facilitate physical and functional mapping of genes and regulatory elements in these large plasmids.

Searched by M. Smith

3/AB/5 (Item 4 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01625601 Genuine Article#: HM836 Number of References: 52
Title: INDUCTION OF DNA AMPLIFICATION IN THE BACILLUS - SUBTILIS CHROMOSOME (Abstract Available)
Author(s): PETIT MA; MESAS JM; NOIROT P; MORELDEVILLE F; EHRLICH SD
Corporate Source: UNIV CALIF BERKELEY,DIV BIOCHEM & MOLEC BIOL/BERKELEY//CA/94720; INRA,INST BIOTECHNOL,GENET MICROBIENNE LAB/F-78352 JOUY EN JOSAS//FRANCE/
Journal: EMBO JOURNAL, 1992, V11, N4 (APR), P1317-1326
Language: ENGLISH Document Type: ARTICLE
Abstract: A system allowing the induction of DNA amplification in Bacillus subtilis was developed, based on a thermosensitive plasmid, pE194, stably integrated in the bacterial chromosome. An amplification unit, comprising an antibiotic resistance marker flanked by directly repeated sequences, was placed next to the integrated plasmid. Activation of pE194 replication led to amplification. Two different amplification processes appeared to take place: one increased the copy number of all sequences in the vicinity of the integrated plasmid and was possibly of the onion skin type, while the other increased the copy number of the amplification unit only and generated long arrays of amplification units. These arrays were purified and shown to consist mainly of directly repeated amplification units but to also contain non-linear regions, such as replication forks and recombination intermediates. They were attached to the chromosome at one end only, and were, in general, not stably inherited, which suggests that they are early amplification intermediates. Longer arrays were detected before the shorter ones during amplification. When the parental amplification unit contained repeats which differed by a restriction site the arrays which derived thereof contained in a majority of cases only a single type of repeat. We propose that the amplified DNA is generated by rolling circle replication, and that such process might underline a number of amplification events.

3/AB/6 (Item 5 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01503859 Genuine Article#: HE193 Number of References: 52
Title: CLONING OF THE COMPLETE BIOSYNTHETIC GENE-CLUSTER FOR AN AMINONUCLEOSIDE ANTIBIOTIC , PUROMYCIN, AND ITS REGULATED EXPRESSION IN HETEROLOGOUS HOSTS (Abstract Available)
Author(s): LACALLE RA; TERCERO JA; JIMENEZ A
Corporate Source: UNIV AUTONOMA MADRID,CSIC,CTR BIOL MOLEC,CANTO BLANCO/E-28049 MADRID//SPAIN/; UNIV AUTONOMA MADRID,CSIC,CTR BIOL MOLEC,CANTO BLANCO/E-28049 MADRID//SPAIN/
Journal: EMBO JOURNAL, 1992, V11, N2 (FEB), P785-792
Language: ENGLISH Document Type: ARTICLE
Abstract: Puromycin, produced by Streptomyces alboniger, is a member of the large group of aminonucleoside antibiotics . The genes pac and dmpM, encoding a puromycin N-acetyl transferase and an O-demethyl puromycin O-methyltransferase, respectively, are tightly linked in the DNA of S. alboniger. The entire set of genes encoding the puromycin biosynthesis pathway was cloned by screening a gene library from S. alboniger, raised in the low copy number cosmid pKC505, with a DNA fragment containing pac and dmpM. Puromycin was identified by biochemical and physicochemical methods, including H-1 NMR, in the producing

transformants. This pathway was located in a single DNA fragment of 15 kb which included the resistance, structural and regulatory genes and was expressed when introduced into two heterologous hosts Streptomyces lividans and Streptomyces griseofuscus. In addition to pac and dmpM, two other genes have been identified in the pur cluster: pacHY, which determines an N-acetylpuromycin hydrolase and prgl, whose deduced amino acid sequence is significantly similar to that of degT, a Bacillus stearothermophilus pleiotropic regulatory gene.

3/AB/7 (Item 6 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01145877 Genuine Article#: GA302 Number of References: 62
Title: COMPLETE PHYSICAL MAP OF THE BACILLUS - SUBTILIS 168-CHROMOSOME CONSTRUCTED BY A GENE-DIRECTED MUTAGENESIS METHOD
Author(s): ITAYA M; TANAKA T
Corporate Source: MITSUBISHI KASEI INST LIFE SCI,DEPT MOLEC BIOL,MICROBIOL LAB,11 MINAMIOOYA/MACHIDA/TOKYO 194/JAPAN/
Journal: JOURNAL OF MOLECULAR BIOLOGY, 1991, V220, N3, P631-648
Language: ENGLISH Document Type: ARTICLE

3/AB/8 (Item 1 from file: 351)
DIALOG(R)File 351:Derwent WPI

014787818
WPI Acc No: 2002-608524/200265
Related WPI Acc No: 2002-608383
XRAM Acc No: C02-172125
Enhancing production of pantothenate , by culturing microorganisms having deregulated methylenetetrahydrofolate biosynthetic pathway and/or deregulated pantothenate biosynthetic pathway
Patent Assignee: OMNIGENE BIOPRODUCTS INC (OMNI-N)
Inventor: HERMANN T; PATTERSON T A; PERO J G; YOCUM R R
Number of Countries: 099 Number of Patents: 001
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200261108	A2	20020808	WO 2002US925	A	20020118	200265	B

Priority Applications (No Type Date): US 2002347638 P 20020111; US 2001262995 P 20010119; US 2001263053 P 20010119
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200261108	A2	E	66	C12P-013/02	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW

Abstract (Basic): WO 200261108 A2
Abstract (Basic):
NOVELTY - Enhancing production of pantothenate , comprising culturing a microorganism having a deregulated methylenetetrahydrofolate (MTF) biosynthetic pathway and/or deregulated pantothenate biosynthetic pathway, is new.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the

following:
(1) a product synthesized by the novel method;
(2) a composition comprising pantothenate produced by the novel method; and
(3) a recombinant microorganism for the enhanced production of pantothenate .
USE - The method is useful for enhanced production of pantothenate (claimed), which serves as a nutritional requirement of mammals, including livestock and humans.
pp; 66 DwgNo 0/7

3/AB/9 (Item 2 from file: 351)
DIALOG(R)File 351:Derwent WPI

014448655
WPI Acc No: 2002-269358/200231
Related WPI Acc No: 2001-218644
XRAM Acc No: C02-079997
Identifying potential antibiotic or antimicrobial agent, comprises contacting composition comprising pantothenate kinase (CoaX) protein with test compound and identifying inhibitor of the CoaX protein
Patent Assignee: OMNIGENE BIOPRODUCTS INC (OMNI-N); PATTERSON T A (PATT-I); YOCUM R R (YOCU-I)
Inventor: PATTERSON T A; YOCUM R R
Number of Countries: 097 Number of Patents: 003
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week
WO 200216601	A2	20020228	WO 2001US26531	A	20010824	200231 B
AU 200185276	A	20020304	AU 200185276	A	20010824	200247
US 20020168681	A1	20021114	US 2000227860	A	20000824	200277
			US 2001813453	A	20010320	

Priority Applications (No Type Date): US 2001813453 A 20010320; US 2000227860 P 20000824
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200216601	A2	E	128	C12N-015/00	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

AU 200185276	A	C12N-015/00	Based on patent WO 200216601
US 20020168681	A1	G01N-033/53	Provisional application US 2000227860

Abstract (Basic): WO 200216601 A2
Abstract (Basic):
NOVELTY - Assays for identifying a (potential) antibiotic comprising contacting an assay composition comprising a pantothenate kinase (CoaX) protein with a test compound, and determining the ability of the test compound to inhibit the activity of the CoaX protein, is new.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following:
(1) an assay for identifying an antibiotic comprising:
(a) contacting an assay composition comprising CoaX with a test compound;
(b) determining the ability of the test compound to bind to the CoaX ;

(c) selecting the test compound as a potential antibiotic based the ability to bind to the CoaX ; and

(d) further determining the ability of the selected compound to inhibit the activity of a Coax , where the compound is identified as a potential antibiotic based on its ability to bind to the CoaX ;

(2) an assay for identifying a potential antibiotic comprising:

(a) contacting an assay composition comprising CoaX with a test compound and pantothenate or a pantothenate analog; and

(b) determining the ability of the test compound to modulate binding of the pantothenate or pantothenate analog to the CoaX , where the compound is identified as a potential antibiotic based on its ability to modulate binding of the pantothenate or pantothenate analog to the CoaX ;

(3) an assay for identifying an antibiotic by employing the method of (2), and further determining the ability of the selected compound to inhibit the activity of a CoaX , where the compound is identified as a potential antibiotic based on its ability to bind to the CoaX ;

(4) identifying compounds which modulate pantothenate kinase activity by contacting a recombinant cell expressing a single pantothenate kinase encoded by a coaX , gene with a test compound, and determining the ability of the test compound to modulate pantothenate kinase activity in the cell;

(5) identifying compounds which modulate pantothenate kinase activity by contacting a recombinant cell expressing a first and second pantothenate kinase, with a test compound and determining the ability of the test compound to modulate pantothenate kinase activity in the cell, where the first or second pantothenate kinase has reduced activity;

(6) an isolated nucleic acid molecule comprising a coaX gene;

(7) an isolated pantothenate kinase protein encoded by a coaX gene;

(8) a recombinant vector comprising an isolated coaX gene;

(9) a recombinant microorganism comprising the vector; and

(10) a recombinant microorganism selected from the PQ861, PA876, YH1 comprising pOTP72, YH1 comprising pOTP73, and YH1 comprising pAN341.

ACTIVITY - Antibiotic ; Antimicrobial.

MECHANISM OF ACTION - Pantothenate kinase modulator.

USE - The method is useful for identifying potential antibiotics . CoaX protein is a valuable target for identifying bactericidal compounds. CoaX modulating agents can be used in an infectious animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent.

pp; 128 DwgNo 0/10

3/AB/10 (Item 3 from file: 351)
DIALOG(R)File 351:Derwent WPI

014448488
WPI Acc No: 2002-269191/200231
XRAM Acc No: C02-079917

Inducing homologous recombination in bacterial and eukaryotic cells comprising target nucleic acid, for cloning and generating transgenic animals, comprises utilizing lambda recombinases and similar proteins

Patent Assignee: US DEPT HEALTH & HUMAN SERVICES (USSH); US NAT INST OF HEALTH (USSH)
Inventor: COPELAND N G; COURT D L; ELLIS H M; JENKINS N A; LEE E; YU D
Number of Countries: 096 Number of Patents: 002
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200214495	A2	20020221	WO 2001US25507	A	20010814	200231	B
AU 200183377	A	20020225	AU 200183377	A	20010814	200245	

Priority Applications (No Type Date): US 2001271632 P 20010226; US 2000225164 P 20000814

Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200214495	A2	E	124	C12N-015/00	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

AU 200183377	A		C12N-015/00	Based on patent WO 200214495

Abstract (Basic): WO 200214495 A2

Abstract (Basic):

NOVELTY - Inducing (I) homologous recombination (HR) in a cell comprising a target nucleic acid (TNA), comprises:

(a) introducing into a cell a first nucleic acid (FNA) comprising a homologous sequence to TNA to induce HR, where the cell comprises a nucleic acid (NAP) encoding a single-stranded DNA binding polypeptide capable of promoting HR; and

(b) inducing expression of NAP to promote HR of FNA with TNA.

DETAILED DESCRIPTION - Inducing (I) homologous recombination (HR) in a cell comprises:

(a) introducing into a cell a FNA comprising a homologous sequence to TNA of sufficient length to induce HR, where the cell comprises a NAP that encodes a polypeptide that functions in double-strand break repair HR, operably linked to a de-repressible promoter; and

(b) inducing expression of NAP to promote HR of FNA with TNA.

INDEPENDENT CLAIMS are also included for the following:

(1) a bacterial cell (II) comprising a defective lambda prophage of genotype lambda cI857 DELTA (cro-bioA); and

(2) a mini-lambda (III) comprising a lambda gene comprising a de-repressible promoter operably linked to a nucleic acid sequence encoding Beta, Exo (exonuclease of lambda) and Gam (a lambda protein involved in double strand break repair HR), a nucleic acid sequence encoding a selectable marker, an attP site and a nucleic acid sequence encoding an integrase, where the lambda genome lacks a replication origin.

USE - (I) is useful for performing HR of a nucleotide sequence of interest, preferably intrachromosomal or extrachromosomal nucleic acid or a nucleic acid located on a bacterial artificial chromosome, a P1 artificial chromosome, plasmid, cosmid or yeast artificial chromosome in a host cell such as eukaryotic (mammalian or stem) cell, or bacterial cell, especially Escherichia coli, which is a host recombination defective strain, such as rec A- strain or rec A+ strain. HR alters a function of a gene in the cell. A mini-lambda (III) is useful for producing a bacterial cell, preferably a E. coli DH10B cell comprising a chromosome with a de-repressible promoter operably linked to a nucleic acid sequence encoding lambda Bet, Gam and Exo, by transforming a bacterial cell comprising a attB site on a chromosome of the bacteria with (III), which integrates (III) into the chromosome, and producing the bacterial cell. (I) is also useful for:

(i) cloning a nucleic acid molecule in a cell;

(ii) subcloning a DNA sequence comprising 20, preferably 80 kb of extrachromosomal DNA; and

(iii) altering a eukaryotic nucleic acid sequence, preferably a mammalian nucleic acid or encoding an epitope tag (claimed);

(iv) generating transgenic and knockout animals;
(v) gene replacement;
(vi) subcloning large DNA fragments without the need for restriction enzymes; and
(vii) repairing single or multiple base mutations to wild type or creating specific mutations in the genome.
A bacterial cell (II) comprising a defective lambda prophage of genotype lambdacI857 DELTA(cro-bioA) is useful for high efficiency HR.
ADVANTAGE - (I) promotes high efficiency HR in bacterial and eukaryotic cells.
pp; 124 DwgNo 0/13

3/AB/11 (Item 4 from file: 351)
DIALOG(R)File 351:Derwent WPI

014374987
WPI Acc No: 2002-195690/200225
XRAM Acc No: C02-060442
Novel food complex made of two emulsions with first solids-in-oil emulsion having bioactive materials forming solid phase and edible oil forming continuous phase (CP), as dispersed phase and hydrocolloid polymer as CP
Patent Assignee: ACUABIOTEC LLC (ACUA-N)
Inventor: MORIARTY D J W; VILLAMAR D F
Number of Countries: 096 Number of Patents: 002
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200200035	A1	20020103	WO 2001US16489	A	20010622	200225	B
AU 200168078	A	20020108	AU 200168078	A	20010622	200235	

Priority Applications (No Type Date): US 2000213538 P 20000623
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200200035	A1	E	38	A23K-001/165	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

AU 200168078	A		A23K-001/165	Based on patent WO 200200035

Abstract (Basic): WO 200200035 A1
Abstract (Basic):
NOVELTY - Bioactive food complex for aquatic animals comprising an emulsion (E1) which is a solids-in-oil or oil-in-solids emulsion of bioactive materials that form solid phase and lipid soluble bioactive compounds dissolved in edible oil, and of a second emulsion comprising oil-in-polymer or solids-in-polymer emulsion with E1 as dispersed phase and hydrocolloid polymer as continuous phase, is new.
DETAILED DESCRIPTION - Bioactive food complex (I) for feeding aquatic animals, comprising:
(1) first emulsion (emulsion-1) (E1) which is solids-in-oil or oil-in-solids emulsion of bioactive materials and powder nutrients that form solid phase and lipid soluble bioactive compounds dissolved in edible oil that form oil phase; and
(2) second emulsion comprising oil-in-polymer or solids-in-polymer emulsion with E1 as dispersed phase and hydrocolloid polymer as continuous phase, where the complex is exposed to ions whereby the hydrocolloid polymer is ionically crosslinked and forms a physically

stable gel matrix with E1 entrapped in the second emulsion, thereby forming bioactive food complex.

INDEPENDENT CLAIMS are also included for the following:

(1) controlling (M1) and/or preventing diseases in aquatic animals by feeding the aquatic animals a composition comprising at least one probiotic bacteria and at least one inhibitory or regulatory compound; and

(2) preparation (M2) of (I), comprising:

(a) forming E1 comprising a solids-in-oil or an oil-in-solids emulsion of bioactive materials and powder nutrients forming the solid phase and lipid soluble bioactive compounds dissolved in edible oil forming the oil phase and of a second emulsion comprising an oil-in-polymer or solids-in-polymer emulsion with the dispersed phase comprising E1 and a hydrocolloid polymer serving as the continuous phase; and

(b) exposing the hydrocolloid polymer to ions, thereby ionically crosslinking the polymer forming a physically stable gel matrix, entrapping E1 in the second emulsion

ACTIVITY - Antibacterial .

No biological data is given.

MECHANISM OF ACTION - Competitive exclusion, direct inhibition of cell-to-cell signaling molecules and direct inhibition of homoserine lactone and (acyl)homoserine lactone regulated processes of pathogenic bacteria.

USE - (I) is useful for feeding aquatic animals. (I) is useful for controlling and/or preventing diseases in aquatic animals caused by gram negative and gram positive bacteria. (M1) is useful for controlling and/or preventing diseases in aquatic animals caused by gram negative bacteria such as Vibrio harveyi, V. parahaemolyticus, V. splendidus, V. mimicus, V.cholerae, V. alginolyticus, V. anguillarum, Vibrio sp. or Aeromonas sp., or gram positive bacteria such as Streptococcus, Carnobacterium or Micrococcus. The pathogens are preferably controlled in the digestive tract of the animals or in the environment of animals including feed bins, feed trays, pens, stands, aquaria, tanks, cages, raceways, ponds, water, surfaces, and sediments of these or other enclosures. (All claimed). (M1) is useful for controlling and/or preventing diseases in crustacean, molluscan, finfish larval, postlarval, juvenile and adult forms. The bacterial pathogenicity is inhibited by a combination of the following mechanisms of the probiotic bacteria such as: control of pathogens by probiotic bacteria by competitive exclusion such as competition for food and space, and by direct inhibition such as by in situ production of antibiotics and gram positive and gram negative bacteria; inhibition of virulence gene expression of gram positive and gram negative pathogenic bacteria by probiotic bacteria; and inhibition of regulation of virulence gene expression in gram negative pathogenic bacteria, by furanones.

ADVANTAGE - The combined effect of probiotic and inhibitory furanone provides most effective control in the hatchery environment and other aquatic environments. The bioactive food compounds provide essential micro and macro nutrients required for normal growth and survival of larval shrimp and eliminate the need to use live and fresh foods.

pp; 38 DwgNo 0/0

3/AB/12 (Item 5 from file: 351)
DIALOG(R)File 351:Derwent WPI

013897048
WPI Acc No: 2001-381261/200140

XRAM Acc No: C01-116753
Pharmaceutical, cosmetic, dietetic or nutritional compositions containing ozonized oil and thioctic acid, useful e.g. for treating or preventing dermatitis, acne, ulcers or effects of oxidative stress
Patent Assignee: DALL'AGLIO R (DALL-I); GOMEZ MORALEDA M (MORA-I); MELEGARI P (MELE-I); DALL' AGLIO R (AGLI-I); MORALEDA M G (MORA-I)
Inventor: DALL'AGLIO R; GOMEZ MORALEDA M; MELEGARI P; DALL' AGLIO R; MORALEDA M G
Number of Countries: 094 Number of Patents: 006
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200137829	A1	20010531	WO 2000ES208	A	20000609	200140	B
AU 200050796	A	20010604	AU 200050796	A	20000609	200153	
ES 2162586	A1	20011216	ES 992602	A	19991125	200212	
ES 2162586	B1	20020701	ES 992602	A	19991125	200253	
EP 1273295	A1	20030108	EP 2000935232	A	20000609	200311	
			WO 2000ES208	A	20000609		
US 20030049333	A1	20030313	WO 2000ES208	A	20000609	200321	
			US 2002155472	A	20020524		

Priority Applications (No Type Date): ES 992602 A 19991125
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200137829	A1	S	33	A61K-031/327	

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW

AU 200050796	A		A61K-031/327	Based on patent WO 200137829
ES 2162586	A1		A61K-031/327	
ES 2162586	B1		A61K-031/327	
EP 1273295	A1	E	A61K-031/327	Based on patent WO 200137829

Designated States (Regional): AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI

US 20030049333	A1		A61K-031/385	CIP of application WO 2000ES208

Abstract (Basic): WO 200137829 A1
Abstract (Basic):

NOVELTY - A novel composition (I) comprises 0.01-99.99 (preferably 0.01-50) wt. % of each of: (a) one or more of ozonized oils and/or other ozonized natural or synthetic products and (b) thioctic acid and/or its derivatives.

ACTIVITY - Dermatological; antiinflammatory; antibacterial ; antiseborrheic; antiulcer; vulnerary.

MECHANISM OF ACTION - Oxygen carrier; antioxidant; antiradical.

USE - (I) is specifically used in pharmaceutical, cosmetic, dietetic or nutritional compositions (all claimed). In particular, (I) is used as a medicament for preventing or treating dermatitis, infections, acne, ulcers (including gastrointestinal ulcers), scars, burns, tissue lesions, cellular dysfunction, energy-producing metabolic disorders and disorders in the enzymatic systems providing protection against oxidation, environmental factors, free radicals, oxidative stress and stress in general, in humans or animals (all claimed).

In tests for the treatment of gastrointestinal ulcers associated with Helicobacter pylori infection, administration of capsules containing 1 g of a mixture of 50 wt. % silica gel, 48 wt. % ozonized oil, 1.9 wt. % thioctic acid and 0.1 wt. % melatonin, at 2 capsules per day for the first 7 days then subsequently at one capsule per day, completely eradicated the ulcers and infection in 8/10 patients within 21 days and in 9/10 patients within 42 days.

ADVANTAGE - The oxygen carrier (a) and the antioxidant (b) each potentiate the beneficial effects of the other component, e.g. in stimulating enzymatic, cellular and metabolic functions.
pp; 33 DwgNo 0/0

3/AB/13 (Item 6 from file: 351)
DIALOG(R)File 351:Derwent WPI

013052110
WPI Acc No: 2000-223965/200019
XRAM Acc No: C00-068247
Composition comprises non-pathogenic lactic acid-producing bacterial species or strains, useful for increasing the solubility and bioavailability of nutritional materials within the gastrointestinal tract
Patent Assignee: GANEDEN BIOTECH INC (GANE-N)
Inventor: FARMER S
Number of Countries: 086 Number of Patents: 004
Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week	
WO 200007606	A2	20000217	WO 99US17671	A	19990806	200019	B
AU 9957719	A	20000228	AU 9957719	A	19990806	200030	
EP 1102595	A2	20010530	EP 99945016	A	19990806	200131	
			WO 99US17671	A	19990806		
JP 2002522393	W	20020723	WO 99US17671	A	19990806	200263	
			JP 2000563291	A	19990806		

Priority Applications (No Type Date): US 99369016 A 19990805; US 9895786 P 19980807
Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200007606	A2	E	43	A61K-035/74	
Designated States (National): AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW					
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW					
AU 9957719	A			A61K-035/74	Based on patent WO 200007606
EP 1102595	A2	E		A61K-035/74	Based on patent WO 200007606
Designated States (Regional): AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
JP 2002522393	W		56	A61K-035/74	Based on patent WO 200007606

Abstract (Basic): WO 200007606 A2
Abstract (Basic):
NOVELTY - Composition comprises one or more non-pathogenic lactic acid-producing bacterial species or strains within a carrier suitable for administration to the gastrointestinal tract of a vertebrate. The species or strain possesses the ability to increase the solubility and bioavailability of nutritional materials within the gastrointestinal tract of an animal or, preferably, a human.
ACTIVITY - None given.
MECHANISM OF ACTION - None given.
USE - The compositions increase the solubility and bioavailability of nutritional materials, preferably vitamins and minerals within the gastrointestinal tract of an animal or human
pp; 43 DwgNo 0/4

3/AB/14 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0290045 DBR Accession No.: 2002-11892 PATENT
Identifying potential antibiotic or antimicrobial agent, comprises contacting composition comprising pantothenate kinase (CoaX) protein with test compound and identifying inhibitor of the CoaX protein - recombinant enzyme gene production, vector expression in bacterium cell for drug screening and disease therapy
AUTHOR: YOCUM R R; PATTERSON T A
PATENT ASSIGNEE: OMNIGENE BIOPRODUCTS INC 2002
PATENT NUMBER: WO 200216601 PATENT DATE: 20020228 WPI ACCESSION NO.: 2002-269358 (200231)
PRIORITY APPLIC. NO.: US 813453 APPLIC. DATE: 20010320
NATIONAL APPLIC. NO.: WO 2001US26531 APPLIC. DATE: 20010824
LANGUAGE: English
ABSTRACT: DERWENT ABSTRACT: NOVELTY - Assays for identifying a (potential) antibiotic comprising contacting an assay composition comprising a pantothenate kinase (CoaX) protein with a test compound, and determining the ability of the test compound to inhibit the activity of the CoaX protein, is new. DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following: (1) an assay for identifying an antibiotic comprising: (a) contacting an assay composition comprising CoaX with a test compound; (b) determining the ability of the test compound to bind to the CoaX ;(c) selecting the test compound as a potential antibiotic based the ability to bind to the CoaX ; and (d) further determining the ability of the selected compound to inhibit the activity of a Coax , where the compound is identified as a potential antibiotic based on its ability to bind to the CoaX ; (2) an assay for identifying a potential antibiotic comprising: (a) contacting an assay composition comprising CoaX with a test compound and pantothenate or a pantothenate analog; and (b) determining the ability of the test compound to modulate binding of the pantothenate or pantothenate analog to the CoaX , where the compound is identified as a potential antibiotic based on its ability to modulate binding of the pantothenate or pantothenate analog to the CoaX ; (3) an assay for identifying an antibiotic by employing the method of (2), and further determining the ability of the selected compound to inhibit the activity of a CoaX , where the compound is identified as a potential antibiotic based on its ability to bind to the CoaX ; (4) identifying compounds which modulate pantothenate kinase activity by contacting a recombinant cell expressing a single pantothenate kinase encoded by a coaX , gene with a test compound, and determining the ability of the test compound to modulate pantothenate kinase activity in the cell; (5) identifying compounds which modulate pantothenate kinase activity by contacting a recombinant cell expressing a first and second pantothenate kinase, with a test compound and determining the ability of the test compound to modulate pantothenate kinase activity in the cell, where the first or second pantothenate kinase has reduced activity;(6) an isolated nucleic acid molecule comprising a coaX gene; (7) an isolated pantothenate kinase protein encoded by a coaX gene; (8) a recombinant vector comprising an isolated coaX gene; (9) a recombinant microorganism comprising the vector; and (10) a recombinant microorganism selected from the PQ861, PA876, YH1 comprising pOTP72, YH1 comprising pOTP73, and YH1 comprising pAN341. BIOTECHNOLOGY - Preferred Assay: The assay composition comprises (partially) purified CoaX protein, and crude cell extracts from a cell producing CoaX protein. The CoaX protein is encoded by a coaX gene derived from a pathogenic bacteria selected from Bordetella pertussis, Xylella fastidiosa, Borrelia burgdorferi, Campylobacter jejuni, Clostridium difficile, Helicobacter pylori, Neisseria

meningitidis, Pseudomonas aeruginosa, Treponema pallidium, Bacillus anthracis and Neisseria gonorrheae. The CoaX protein has a fully defined sequence of 258, 250, 265, 272, 258, 255, 262, 246, 273, 262, 229, 257, 223, 267, 248, 209, 592, 460, 244, 592, 262, 254, 258, 260, 257, 256, 219, 212, 249, 241, 242, 223, or 249 amino acids as given in the specification. The CoaX protein is encoded by a coaX gene derived from a bacteria further selected Aquifex aeolicus, Bacillus anthracis, Bacillus halodurans, Bacillus stearothermophilus, Bacillus subtilis , Caulobacter crescentus, Chlorobium tepidum, Clostridium acetobutylicum, Dehalococcoides ethenogenes, Deinococcus radiodurans, Desulfovibrio vulgaris, Geobacter sulfurreducens, Pseudomonas putida, Rhodobacter capsulatus, Thiobacillus ferrooxidans, Streptomyces coelicolor, Synechocystis sp., Thermotoga maritima, Bordetella pertussis, Borrelia burgdorferi, Campylobacter jejuni, Clostridium difficile, Helicobacter pylori, Neisseria meningitidis, Neisseria gonorrheae, Porphyromonas gingivalis, Pseudomonas aeruginosa, Treponema pallidium, Xelella fastidiosa and Mycobacterium tuberculosis. The composition is further contacted with pantothenate or a pantothenate analog, where the ability to modulate activity of CoaX is determined based on the ability of the test compound to effect level s of pantothenate or pantothenate analog in the assay mixture. The first pantothenate kinase is encoded by a coaA gene and the second pantothenate kinase is encoded by a coaX gene, or the first pantothenate kinase is encoded by a coaX gene and the second pantothenate kinase is encoded by a coaA gene. Determining the ability of the test compound to modulate pantothenate kinase activity in the cell comprises determining the ability of the test compound to inhibit pantothenate kinase activity. Preferred Cell: The recombinant cell is a Gram negative or Gram-positive microorganism. Preferred Microorganism: The microorganism is of the genus Bacillus or Escherichia, specifically Bacillus subtilis or Escherichia coli. ACTIVITY - Antibiotic ; Antimicrobial. MECHANISM OF ACTION - Pantothenate kinase modulator. USE - The method is useful for identifying potential antibiotics . CoaX protein is a valuable target for identifying bactericidal compounds. CoaX modulating agents can be used in an infectious animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. EXAMPLE - None given in the source material.(128 pages)

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